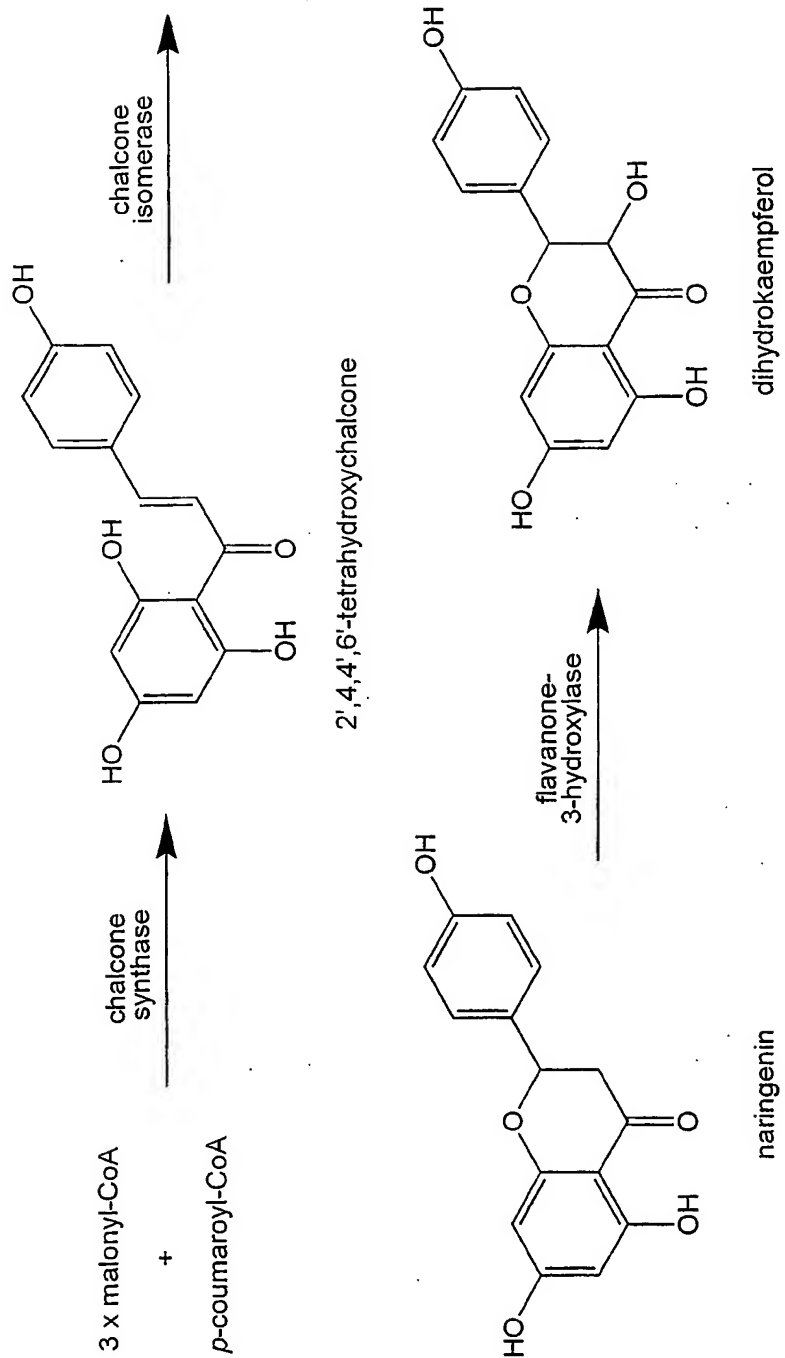


Figure 1A



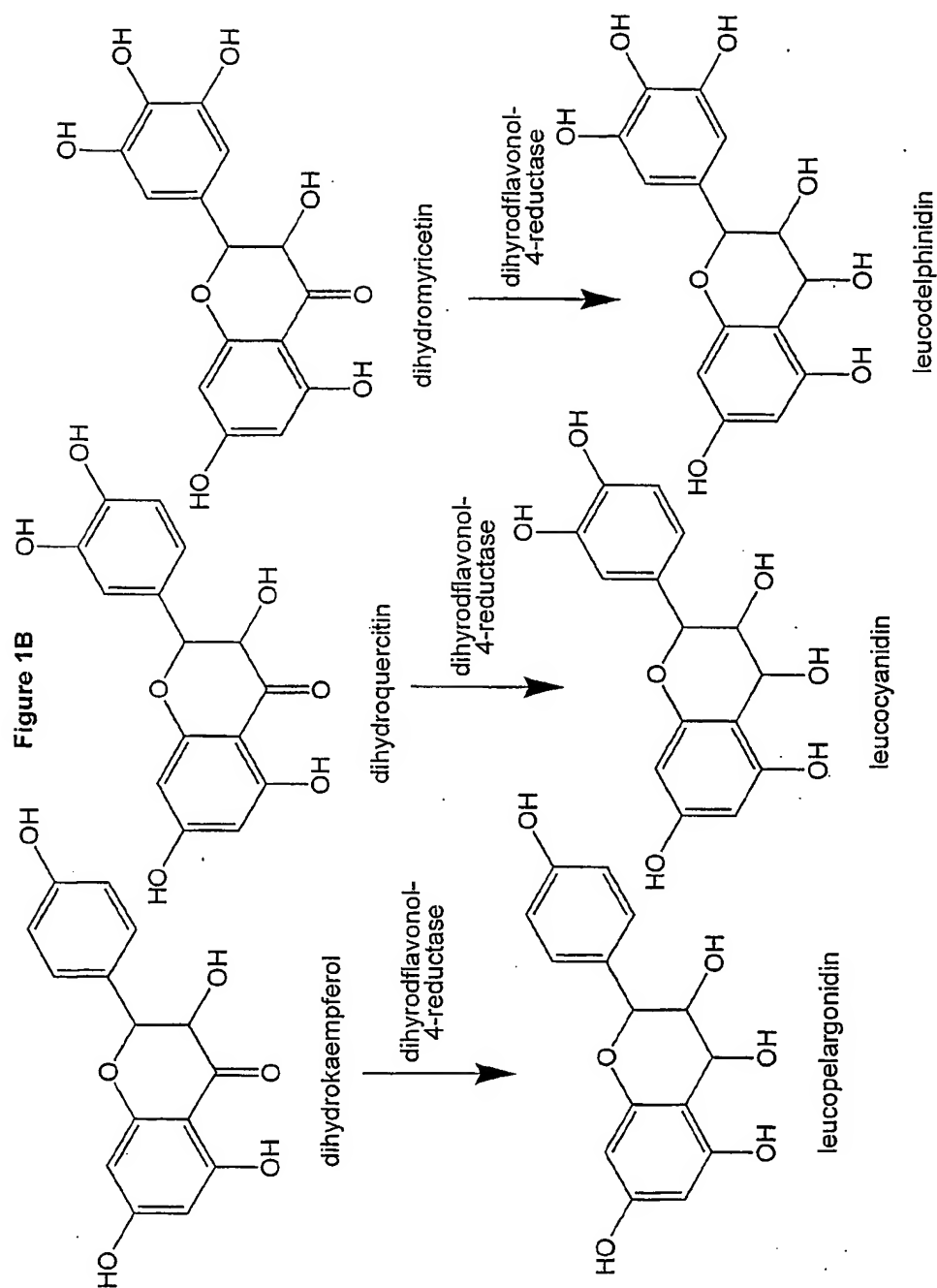


Figure 2B

SEQ ID NO: 4	190	200	210	220	230	240	227
SEQ ID NO: 6	AWKFAKEHGMDF	AIIPALVIGP	PELLPTMP	SSVISALS	PINGIEAH	YSIIKQAQ	227
SEQ ID NO: 8	AWKFAKEHGMDF	AIIPALVIGP	PELLPTMP	SSVISALS	PINGIEAH	YSIIKQAQ	156
SEQ ID NO: 17	AWKFAKEHGMDF	AIIPALVIGP	PELLPTMP	SSVISALS	PINGIEAH	YSIIKQAQ	227
SEQ ID NO: 18	AWKFAKEHGMDF	AIIPALVIGP	PELLPTMP	SSVISALS	PINGIEAH	YSIIKQAQ	239
SEQ ID NO: 4	250	260	270	280	290	300	286
SEQ ID NO: 6	-FVHIEDICLAH	IFLFEQPKA	EGRYICSAC	DVTIHDIVK	LINEKYPE	KVPTKFNIPDQ	286
SEQ ID NO: 8	-FVHIEDICLAH	IFLFEQPKA	EGRYICSAC	DVTIHDIVK	LINEKYPE	KVPTKFNIPDQ	216
SEQ ID NO: 17	SITHVEDICRA	QIFVAEKE	SASGRYIC	CAHNTSV	PELAKFL	SKRYPQYKIPTEFDDCPSK	286
SEQ ID NO: 18	-FVHLDLCLAH	IFLFEQPKA	EGRYICSAC	DVTIHDIVK	LINEKYPE	KVPTKFNIPDQ	299
SEQ ID NO: 4	310	320	330	340	350	360	337
SEQ ID NO: 6	LEPVRFSKKIT	DLGQFKYS	LEDMYTGA	IDTCIEK	GLLPKPAE	-----IPANGIE	337
SEQ ID NO: 8	LEPVRFSKKIT	DLGQFKYS	LEDMYTGA	IDTCIEK	GLLPKPAE	-----IPANGIE	255
SEQ ID NO: 17	AKLIISSEKLV	KEGFSFKY	GIEEYDQ	TEYLKSGAL	-----N--	-----	345
SEQ ID NO: 18	LELVRFSKKIT	DLGQFKYS	LEDMYTGA	IDTCRDK	GLLPKPAE	GGLFTKPGETPVNAM	340
	-PKLTLSQK	LINEGFR	EYGINEMY	DOMIEYFES	KGLI-----	-----KAK	

Figure 2C

SEQ ID NO:4	--	339
SEQ ID NO:6	--	339
SEQ ID NO:8	HK	256
SEQ ID NO:17	-N	347
SEQ ID NO:18	HK	342
	ES	

Figure 3A

SEQ ID NO:12	M-DGNKGPVVVTGASGFVGSWLVNKLQVGYTVRATVRDPANVEKNKPLLELPGAKERLS	59
SEQ ID NO:14	MANTSKGKVCVTGASGFVASWLVKRLLESGYHVLGTVRDPGNQKKVAHLNLAGAKEGLE	60
SEQ ID NO:16	M-DGSKGPVVVTGASGFVGSWLVNKLQVGYTVRATVRDPANVEKNKPLLELPGAKERLS	59
SEQ ID NO:19	M-DGNKGPVVVTGASGFVGSWLVNKLQVGYTVRATVRDPANVEKTKPLLELPGAKERLS	59
SEQ ID NO:20	MVISSKGKVCVTGASGFVASWLVKRLLEAGYHVIGTVRDPNSREKVSHLWRLPSAKERLQ	60
SEQ ID NO:12	IWKADLSEEGSFDDAIAAGCTGVFHVATPMDFDSQDP-ENEVIKPTVEGMLSINMRACKEAG	118
SEQ ID NO:14	LVRADLLEEGSFDDAVMACEGVFHTASPIITNADS--KEEMLDSAINGTLNVLRSCKKNP	118
SEQ ID NO:16	IWKADLSEEGSFDDAIAAGCTGVFHVATPMDFDSKDP-ENEVIKPTVEGMLSINMRACKEAG	118
SEQ ID NO:19	IWKADLSEEGSFNEAIAAGCTGVFHVATPMDFDSQDP-ENEVIKPTVEGMLSINMRACKEAG	118
SEQ ID NO:20	LVRADLMEEGSFDDAVMACEGVFHTASPVLAKSDSNCKEEMLVPAINGTLNVLKSCCKNP	120
SEQ ID NO:12	TVKRIVFTSSAGSVNIEE----RQRPAYDQDNWSDIDFCRRVKMTGWMYFVSKSLAEKAA	174
SEQ ID NO:14	FLKRVVLTSSSSTMRLRDEAEFPNVLIDETSWSSVEFCESIQI--W-YAVAKILAEKSA	175
SEQ ID NO:16	TVKRIVFTSSAGSVNIEE----RQRPAYDQDNWSDIDFCRRVKMTGWMYFVSKSLAEKAA	174
SEQ ID NO:19	TVKRIVFTSSAGSVNIEE----RPRPAYDQDNWSDIDYCRRVKMTGWMYFVSKALAEKAA	174
SEQ ID NO:20	FLKRVVLTSSSSTVRIMDESK-HPEISLDETIWSSVALCEKIQI--W-YALAKISAEKAA	176

Figure 3B

SEQ ID NO:12	MEYASENGLDFISIIPTLVVGPFLSAGMPPSLVLTALALITGNEAHYSILKQVQLVHLLDL	234
SEQ ID NO:14	WEFAKENNIDLVAVLPTFIIGPNLSPVLGPTASDVGLGFKGETEKFTIFGRMGYVHIDDV	235
SEQ ID NO:16	MEYASENGLDFISIIPTLVVGPFLSAGMPPSLVLTALALITGNEAHYSILKQVQLVHLLDL	234
SEQ ID NO:19	MEYASENGLDFISIIPTLVVGPFLSAGMPPSLVLTALALITGNEAHYSILKQVQLVHLLDL	234
SEQ ID NO:20	WEFAKENNIDLVTVLPSFVIGPSLSHLSVTASDILGLLQGLTDRFISYGRMGYVHIDDV	236
SEQ ID NO:12	CDAMTFLFEHPEANGRYICSSHDATIHGLARMLRDRFPEYSIPQKFAGVDDDLQPIHFSS	294
SEQ ID NO:14	ASCHILVYETADAKGRYICNSAVLDSNELVALLAKRFPSPFIPKSLPNIYGE-QTYGYNT	294
SEQ ID NO:16	CDAMTFLFEHPEANGRYICSSHDATIHGLARMLRDRFPEYSIPHKFAGVDDDLQPIHFSS	294
SEQ ID NO:19	CDAMTFLFEHPEANGRYICSSHDATIHGLARMLQDRFPEYDIPQKFAGVDDNLQPIHFSS	294
SEQ ID NO:20	ASCHILVYEAPOATGRYLCNSVVLNNELVALLAKQFPIFPIPRSLRNPYEK-QSYELNT	295
SEQ ID NO:12	KKLLDHGFSFRYTAEDMFDAAIRTCREKGLIPLGDAPPAAGGKLGALAAGEGQAIGAET	354
SEQ ID NO:14	SKIRKLGLEFR-GVEEMFDDSVESILKAHGYL-----REGAA	329
SEQ ID NO:16	KKLLDHGFSFRYTAEDMFDAAIRTCREKGLIPLGDAPAPAAAAGKLGALAAGKGAIGAET	354
SEQ ID NO:19	KKLLDHGFSFRYTTEDMFDAAIHTCRDKGLIPLGDVPAPAAAGKLGALAAGEGQAIGAET	354
SEQ ID NO:20	SKIQQLGFKFK-GVQEMFGDCVESLKDQGH-----LECPL	330

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